Detection and utility of ancestral haplotypes in cattle breeds

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Detection and utility of ancestral haplotypes in cattle breeds

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Application The study of ancestral haplotypes identifies regional variants of potential interest in selection programmes to improve productivity and fitness. It also provides information regarding population history to be used in management.

Introduction In cattle, intense selection has led to the development of strong linkage disequilibrium with different patterns across breeds. The analysis of ancestral haplotypes is expected to provide information about the evolutionary history of diverse populations and identify regions of common interest for both conservation and breeding programmes. The main objective of the present study was to develop a simple procedure to detect ancestral haplotypes in populations with genetic links. The procedure was applied to Fleckvieh, Simmental and Brown-Swiss population data. Regions of common interest were identified and patterns of the population history and dynamics were assessed.

Material and methods
Fleckvieh/Simmental dataset: 473 bulls genotyped for 714,759 Single Nucleotide Polymorphisms (SNPs) with Fleckvieh (315 bulls) and Simmental (158 bulls) being treated as different populations with up to 7 generations.
Brown-Swiss dataset: 412 bulls genotyped for 714,759 SNPs and with each of the five involved countries considered as a different population: Austria (21 bulls. 6 generations), Germany (54 bulls. 6 generations), Italy (77 bulls. 7 generations), Switzerland (184 bulls. 7 generations) and USA (77 bulls. 7 generations).
Analysis: Genotypes were phased using clusters of 100 SNPs. Within each population, haplotypes in the base (oldest) generation were identified in each cluster and considered as ancestral. In subsequent generations, ancestral haplotype frequency and average similarity (molecular co-ancestry) was estimated and averaged across all clusters. Linear regression was used to assess trends in frequency and co-ancestry across time. Haplotype variability was computed as the average number of haplotypes identified per cluster, and ancestral haplotypes identified in a given population were also traced in others to assess the shared percentage.

Results A higher haplotype variability (71.55) and reduced co-ancestry trend ($b=7.43x10^{-5}$) was observed for Fleckvieh than for Simmental (44.98 and $b=4.18x10^{-4}$, respectively). This is contrary to what might have been expected from the origin of Fleckvieh (imported nucleus of Simmental cattle into Germany and Austria). Possible explanations are the enrichment of Simmental haplotypes with local breed haplotypes during the formation of the Fleckvieh breed and an unbalanced genetic flow between the two populations. Both explanations are concordant with the history of Fleckvieh.
The Brown-Swiss breed originated in Switzerland and was exported to USA in 1869, where it was intensively selected and exported back into Italy, Germany and Austria. In concordance, the Swiss population showed the highest variability (37.22) and a low proportion of shared ancestral haplotypes with other European populations (5.8% ± 1.09), but also a high shared proportion with the USA population (33.19%). Furthermore, the non-Swiss European populations and the USA population had similar proportions of shared ancestral haplotypes (9.33% ± 1.76 and 11.58% ± 1.98, respectively).
The analysis of the most common ancestral haplotypes (Table 1) also revealed selection signatures in the populations, in agreement with previous studies (Mészáros *et al*., 2015; Stella *et al*., 2010) and showing interesting genes closer than 0.3 Mb of the most frequent haplotypes.

Table 1 Analysis of the top 5 common ancestral haplotypes in Fleckvieh (Fleck), Simmental (Sim) and Brown-Swiss (BS)

Chr	Breeds (number of haplotypes)	Related genes (function)
5	Sim (2), BS (2)	SYT10 (longevity/maturity), PMEL and ERBB5 (coat colour)
6	Fleck (3), Sim (3), BS (5)	MEP6, ISBP, LAP3, MED28 (milk protein/fat) and KIT (coat colour)
7	Fleck (2)	Previous QTL detected for milk production
21	BS (1)	MEF2A (milk production)

Conclusion Detection of ancestral haplotypes has led to the identification of signatures of selection in three common cattle breeds, mirroring also their population dynamics.

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